

Mar 11 07:37:31 2002

pct-us01-47576-347.rng

Page 3

AC A236150:
XX 11-FEB-2000 (first entry)
XX DNA encoding cancer associated antigen KOC-1.
XX Cancer associated antigen: KOC-1; cancer: vaccine; CT7, ss.
XX Homo sapiens.
XX MO954738-A1.
XX 28-OCT-1999.
XX 16-MAR-1999; 99MO-US05766.
XX 17-APR-1998; 98US-0061709.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Chen Y, Gure A, Tsang S, Stockert E, Jager E, Knuth A, Old LJ;
XX MPI; 2000-013284/01.
XX Nucleotides representing cancer-associated genes, used to develop
XX products for the diagnosis, monitoring and treatment of cancers
XX
XX Claim 88: Page 39-40; 44pp: English.
XX
XX The present sequence represents a cancer associated antigen gene
XX designated KOC-1. The specification also describes a cancer associated
XX antigen designated CT7. The CT7 polynucleotide was isolated from
XX SK-MEL-37 melanoma cells. The polypeptide has some homology with
XX MAGE-10, limited to about 210 carboxy terminal amino acids. The amino
XX terminal of the protein has a repetitive pattern, with repeats rich in
XX serine, proline, glutamine and leucine, and an almost invariable core of
XX the peptide given in A474387. The CT7 polypeptide can be processed to
XX peptides which provoke lysis by cytolytic T cells. The polynucleotides
XX and polypeptides can be used for treating a cancerous condition and
XX screening for or diagnosing cancerous conditions. The cancer associated
XX antigen can be used as an immunogenic or vaccine composition with an
XX adjuvant, e.g., a cytokine, a saponin, or granulocyte macrophage-colony
XX stimulating factor (GM-CSF).
XX
XX Sequence 4159 BP; 1281 A; 830 C; 851 G; 1181 T; 16 other:
SQ
Query Match 99.8% Score 1736.8; DB 21; Length 4159;
Best Local Similarity 99.9% Pred. No. 0;
Matches 1738; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 551 ctatgccatctatgagatgctgagagctgagcaagtgaaactgactcgaaactgca 610
Oy 361 gttgttaaatgtaactctatccagtgaaagcagagctagacagactagacaaactgaa 420
Db 611 gttgttaaatgtaactctatccagtgaaagcagagctagacagactagacaaactgaa 670
Oy 421 ggaattcagtgaaagacttcacactgtaagagtgagctatccctgtgaaagcgccgac 480
Db 671 ggaattcagtgaaagacttcacactgtaagagtgagctatccctgtgaaagcgccgac 730
Oy 481 cagcaaaaccccttgacagagcccgagagctgagcgggagcttgagcagagagcgccca 540
Db 731 cagcaaaaccccttgacagagcccgagagctgagcgggagcttgagcagagagcgccca 790
Oy 541 aggcagaggtctccagagatccgtatccagcagaaacatgtgattgctctgcgctg 600
Db 791 aggcagaggtctccagagatccgtatccagcagaaacatgtgattgctctgcgctg 850
Oy 601 ctggtcccaacccaattgttgagccatcatagaaagagtgccacatccgaaac 660
Db 851 ctggtcccaacccaattgttgagccatcatagaaagagtgccacatccgaaac 910
Oy 661 atcccaaaacagagccagctcctaagatgctcaccgctaaagaaatgaggggctgct 720
Db 911 atcccaaaacagagccagctcctaagatgctcaccgctaaagaaatgaggggctgct 970
Oy 721 gagaagtgattctactctctactcctacccagagagcactctgcggtctgaactatc 780
Db 971 gagaagtgattctactctctactcctacccagagagcactctgcggtctgaactatc 1030
Oy 781 ctgagagatcatgataagaaagctcagagataaaattcaacagaaagatcccttgaa 840
Db 1031 ctgagagatcatgataagaaagctcagagataaaattcaacagaaagatcccttgaa 900
Oy 841 attcttagcatataaactttctgagagctcattgtaagaaagaaagaaactcttaa 960
Db 1091 attcttagcatataaactttctgagagctcattgtaagaaagaaagaaactcttaa 1150
Oy 901 aaatttgagcagagcagacacataaactcagagatctcccttgagagatctgcgctg 960
Db 1151 aaatttgagcagagcagacacataaactcagagatctcccttgagagatctgcgctg 1210
Oy 961 tataattcagaaagcactatctacgttcaagagcaatgctgagacatgctcacaagctgag 1020
Db 1211 tataattcagaaagcactatctacgttcaagagcaatgctgagacatgctcacaagctgag 1070
Oy 1021 gaggagatcatgaaagaaatcagagagctctctagaaatgataatgctctctatgaaactc 1080
Db 1271 gaggagatcatgaaagaaatcagagagctctctagaaatgataatgctctctatgaaactc 1330
Oy 1081 caagcacttaattctctgagatataatctgaaagccttggtgctgtctccacccaacttca 1140
Db 1331 caagcacttaattctctgagatataatctgaaagccttggtgctgtctccacccaacttca 1390
Oy 1141 ggaatgacacctccacacccaagggccctctcagacatgactccctccacccaagctt 1200
Db 1391 ggaatgacacctccacacccaagggccctctcagacatgactccctccacccaagctt 1450
Oy 1201 gaggcaatcagaagaaagagagctgttacttctgttaccagcactatcaagctcggtgcaatc 1260
Db 1451 gaggcaatcagaagaaagagagctgttacttctgttaccagcactatcaagctcggtgcaatc 1510
Oy 1261 atcggcaagcgggagcagacatcaatcaagcagcttccgcttgcgtgagactcaatgaag 1320
Db 1511 atcggcaagcgggagcagacatcaatcaagcagcttccgcttgcgtgagactcaatgaag 1570
Oy 1321 atggtccagcgggagcagacatgctaaagtgaagatggtgataatcaatcagagcaca 1380
Db 1571 atggtccagcgggagcagacatgctaaagtgaagatggtgataatcaatcagagcaca 1630
Oy 1381 gaggctcaggtcagagctcagaggaagaaattcagagaaatcagaggaagaaacttgctt 1440
Db 1631 gaggctcaggtcagagctcagaggaagaaattcagagaaatcagaggaagaaacttgctt 1690

| XX | Sequence | 4181 BP | 1303 A | 830 C | 851 G | 1181 T | 16 other: |
|-----------------------|--------------|--|------------|-------|--------|--------|-----------|
| Query Match | 99.8% | Score | 1736.0 | DB | 21 | Length | 4181 |
| Best Local Similarity | 99.9% | Pred. No. 0 | | | | | |
| Matches 1738 | Conservative | 0 | Mismatches | 2 | Indels | 0 | Gaps |
| OY | 1 | atgagcaaaactgtatcatcgcaaaaccccaagcgaaagcgcccccctcgagactaaagaat | 60 | | | | |
| DB | 251 | atgagcaaaactgtatcatcgcaaaaccccaagcgaaagcgcccccctcgagactaaagaat | 310 | | | | |
| OY | 61 | atcttcagaagaaacgaaagataatcccggtgtctgggaagccctctctgttgaagactgtctacgcg | 120 | | | | |
| DB | 311 | atcttcagaagaaacgaaagataatcccggtgtctgggaagccctctctgttgaagactgtctacgcg | 370 | | | | |
| OY | 121 | ctctgtgactgtgcccggaacgaaagactgtggccctcacaagagccatcgaaagcgcttcaggttaa | 180 | | | | |
| DB | 371 | ctctgtgactgtgcccggaacgaaagactgtggccctcacaagagccatcgaaagcgcttcaggttaa | 430 | | | | |
| OY | 181 | atagaaactgtgcacgagaaaccccatatagaaggtgtgagccctctggtccccaataaagcgaaagatc | 240 | | | | |
| DB | 431 | atagaaactgtgcacgagaaaccccatatagaaggtgtgagccctctggtccccaataaagcgaaagatc | 490 | | | | |
| OY | 241 | cggaaaaacttcagatacgaataatcccgccctccatcaagtgagaggtgtctgtgataattta | 300 | | | | |
| DB | 491 | cggaaaaacttcagatacgaataatcccgccctccatcaagtgagaggtgtctgtgataattta | 550 | | | | |
| OY | 301 | ctctgactcgaatctgagatgtgtgtggaagacgtcttgagccaaatgaaacccgtactcggaaatctga | 360 | | | | |
| DB | 551 | ctctgactcgaatctgagatgtgtgtggaagacgtcttgagccaaatgaaacccgtactcggaaatctga | 610 | | | | |
| OY | 361 | gtgtgaaatgtgaacccatcttcacgaaagggccaaagcctatgacaagacatacgaacataactgatat | 420 | | | | |
| DB | 611 | gtgtgaaatgtgaacccatcttcacgaaagggccaaagcctatgacaagacatacgaacataactgatat | 670 | | | | |
| OY | 421 | ggatttcagttatgaagaatttcacactgtgaagaatgagcctatataccctctgaaatgagacgagcc | 480 | | | | |
| DB | 671 | ggatttcagttatgaagaatttcacactgtgaagaatgagcctatataccctctgaaatgagacgagcc | 730 | | | | |
| OY | 481 | cagcagaaaaacccctctgcagcagaccccgcgaaggtctgcgcgggggctctgtgacaaaggggctcccta | 540 | | | | |
| DB | 731 | cagcagaaaaacccctctgcagcagaccccgcgaaggtctgcgcgggggctctgtgacaaaggggctcccta | 790 | | | | |
| OY | 541 | aagcaggggtctctcaagagatcgcgtatccaaagcgaaacacatgcatatttgcctctcgtgcgctg | 600 | | | | |
| DB | 791 | aagcaggggtctctcaagagatcgcgtatccaaagcgaaacacatgcatatttgcctctcgtgcgctg | 850 | | | | |
| OY | 601 | ctgtgtccccaaccccatctgtgtgagacacacataagaaagaaagatgtgcccacatcttggaaac | 660 | | | | |
| DB | 851 | ctgtgtccccaaccccatctgtgtgagacacacataagaaagaaagatgtgcccacatcttggaaac | 910 | | | | |
| OY | 661 | atcaccaaaaacgaaacacagatccaaataatgaaatgtgcaccccgataaabaataatgtgcggggcgctg | 720 | | | | |
| DB | 911 | atcaccaaaaacgaaacacagatccaaataatgaaatgtgcaccccgataaabaataatgtgcggggcgctg | 970 | | | | |
| OY | 721 | gaaagatctgatatctatctctctcaccacccctgaaagggcccccctgtgagacttatat | 780 | | | | |
| DB | 971 | gaaagatctgatatctatctctctcaccacccctgaaagggcccccctgtgagacttatat | 1030 | | | | |
| OY | 781 | ctggaagatataatgataaagaaagccaaagatataaaatattcaaaagaaagaaatctccctgaaag | 840 | | | | |
| DB | 1031 | ctggaagatataatgataaagaaagccaaagatataaaatattcaaaagaaagaaatctccctgaaag | 1090 | | | | |
| OY | 841 | attcttgctctcataaataactctgttgagcgctcttatgtgtaaaagaaagaaatctctaa | 900 | | | | |
| DB | 1091 | attcttgctctcataaataactctgttgagcgctcttatgtgtaaaagaaagaaatctctctaa | 1150 | | | | |
| OY | 901 | aaaaactgagcaagaaacagacacataaaatacagaaatctcccatctgcagaaatgtgacgctg | 960 | | | | |
| DB | 1151 | aaaaactgagcaagaaacagacacataaaatacagaaatctcccatctgcagaaatgtgacgctg | 1210 | | | | |
| OY | 961 | tataaactcgaagaaacacattacagtttaaaaggcaatgtgtgagacatgtgccaagacgtcga | 1020 | | | | |